



Inventor Name Search

Enter the **first few letters** of the Inventor's Last Name.
Additionally, enter the **first few letters** of the Inventor's First name.

Last Name**First Name**

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Inventor Name Search

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Last Name**First Name**

Ward

Michael

Search

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Last Name**First Name**

Salohei

Ma

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SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450 5_copy_84_147.rai.

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This page gives you Search Results detail for the Application 10663450 and Search Result us-10-663-450_5_copy_84_147.rai.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:41:45 ; Search time 29.44 Seconds
(without alignments)
190.284 Million cell updates/sec

Title: US-10-663-450-5_COPY_84_147
Perfect score: 323
Sequence: 1 EKKPVKKRKSQVLPEPKT.....NRRAAQSSRERKRLEVEALE 64

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length	DB	ID		Description

1	307	95.0	409	2	US-09-533-029-104	Sequence 104, App
2	174	53.9	248	2	US-09-248-796A-18840	Sequence 18840, A
3	99	30.7	143	2	US-09-640-211A-1930	Sequence 1930, Ap
4	89	27.6	23	2	US-09-831-642-72	Sequence 72, Appl
5	89	27.6	371	2	US-09-148-545-259	Sequence 259, App
6	89	27.6	371	2	US-09-621-011-259	Sequence 259, App
7	86	26.6	102	2	US-09-640-211A-1046	Sequence 1046, Ap
8	82.5	25.5	611	2	US-09-216-393B-81	Sequence 81, Appl
9	81	25.1	212	2	US-09-489-039A-13074	Sequence 13074, A
10	80.5	24.9	395	2	US-09-247-155-113	Sequence 113, App
11	80.5	24.9	395	2	US-09-513-999C-14	Sequence 14, Appl
12	80.5	24.9	395	2	US-09-471-276-14	Sequence 14, Appl
13	80.5	24.9	395	2	US-09-903-190-113	Sequence 113, App
14	80	24.8	63	2	US-09-107-433-3674	Sequence 3674, Ap
15	78	24.1	551	2	US-08-796-899-29	Sequence 29, Appl
16	77.5	24.0	501	2	US-09-949-016-11281	Sequence 11281, A
17	77	23.8	264	2	US-09-949-016-10789	Sequence 10789, A
18	76.5	23.7	351	2	US-09-870-089B-2	Sequence 2, Appli
19	76.5	23.7	362	2	US-09-949-016-10923	Sequence 10923, A
20	75.5	23.4	463	2	US-09-345-236B-2	Sequence 2, Appli
21	75	23.2	170	2	US-09-248-796A-27838	Sequence 27838, A
22	73.5	22.8	260	2	US-09-538-092-950	Sequence 950, App
23	73.5	22.8	338	1	US-08-218-686-2	Sequence 2, Appli
24	73.5	22.8	338	2	US-08-460-242-2	Sequence 2, Appli
25	73.5	22.8	2058	2	US-09-949-016-6835	Sequence 6835, Ap
26	73.5	22.8	2111	2	US-09-949-016-10199	Sequence 10199, A
27	73	22.6	325	2	US-09-267-031-14	Sequence 14, Appl
28	72.5	22.4	521	1	US-08-721-684C-2	Sequence 2, Appli
29	72.5	22.4	521	1	US-09-005-970-2	Sequence 2, Appli
30	72.5	22.4	521	2	US-09-407-715-2	Sequence 2, Appli
31	71.5	22.1	307	2	US-09-267-031-6	Sequence 6, Appli
32	71.5	22.1	1695	2	US-09-866-108A-15753	Sequence 15753, A
33	71	22.0	196	2	US-09-640-211A-881	Sequence 881, App
34	71	22.0	582	2	US-09-976-594-733	Sequence 733, App
35	71	22.0	645	2	US-09-949-016-11022	Sequence 11022, A
36	71	22.0	667	2	US-09-248-796A-14492	Sequence 14492, A
37	71	22.0	700	2	US-09-831-642-34	Sequence 34, Appl
38	71	22.0	1637	2	US-09-718-692-2	Sequence 2, Appli
39	71	22.0	1637	2	US-09-718-852-2	Sequence 2, Appli
40	71	22.0	1637	2	US-09-718-815-2	Sequence 2, Appli
41	70.5	21.8	245	2	US-09-640-211A-833	Sequence 833, App
42	70.5	21.8	452	2	US-09-949-016-7289	Sequence 7289, Ap
43	70.5	21.8	472	2	US-09-520-781-22	Sequence 22, Appl
44	70.5	21.8	472	2	US-09-957-187-22	Sequence 22, Appl
45	70.5	21.8	472	2	US-09-991-053-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-09-533-029-104

; Sequence 104, Application US/09533029

; Patent No. 6664446

; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline

; APPLICANT: Broun, Pierre

; APPLICANT: Riechmann, Jose-Luis

; APPLICANT: Keddie, James

; APPLICANT: Pineda, Omaira

; APPLICANT: Adam, Luc

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Run on:      June 28, 2006, 01:26:15 ; Search time 133.12 Seconds
              (without alignments)
              219.816 Million cell updates/sec
```

```
Title:          US-10-663-450-5_COPY_84_147
Perfect score: 323
Sequence:      1  EKPPVKRKRKSWGQVLPEPKT.....NRRAQSSRRERKRLEVEALE 64
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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```

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

```

```
Database :      A_Geneseq_8:*
1:  geneseqp1980s:*
2:  geneseqp1990s:*
3:  geneseqp2000s:*
4:  geneseqp2001s:*
5:  geneseqp2002s:*
6:  geneseqp2003as:*
7:  geneseqp2003bs:*
8:  geneseqp2004s:*
9:  geneseqp2005s:*
10: geneseqp2006s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	323	100.0	64	5	AAE15373	Aae15373 Trichoder
2	323	100.0	450	4	AAB82975	Aab82975 Trichoder
3	323	100.0	451	5	AAE15371	Aae15371 Trichoder
4	323	100.0	451	8	ADS12801	Ads12801 Trichoder
5	323	100.0	451	8	ADS12804	Ads12804 Trichoder
6	307	95.0	409	7	ABO43144	Abo43144 A. thalia
7	307	95.0	409	7	ADB31925	Adb31925 Plant (A.
8	307	95.0	409	8	ADO02271	Ado02271 Thalecres
9	292	90.4	342	4	AAB82977	Aab82977 Aspergill
10	292	90.4	342	5	AAE15381	Aae15381 Aspergill
11	292	90.4	342	8	ADS12818	Ads12818 Aspergill
12	292	90.4	386	5	AAE15379	Aae15379 Aspergill
13	292	90.4	386	8	ADS12815	Ads12815 Aspergill
14	288	89.2	64	5	AAE15374	Aae15374 Aspergill
15	288	89.2	349	8	ADS12805	Ads12805 Aspergill
16	288	89.2	349	8	ADS12803	Ads12803 Aspergill
17	288	89.2	349	8	ADS12863	Ads12863 Aspergill
18	288	89.2	350	4	AAB82976	Aab82976 Aspergill
19	288	89.2	350	5	AAE15372	Aae15372 Aspergill
20	175	54.2	68	5	AAE15382	Aae15382 Yeast HAC
21	175	54.2	68	8	ADS12859	Ads12859 Saccharom
22	175	54.2	84	5	ABP02534	Abp02534 Human ORF
23	175	54.2	200	8	ADS43437	Ads43437 Bacterial
24	175	54.2	230	2	AAW53806	Aaw53806 Transcrip
25	175	54.2	230	8	ADT87049	Adt87049 Yeast Str
26	175	54.2	238	2	AAW53807	Aaw53807 Transcrip
27	108	33.4	192	4	AAB82614	Aab82614 Maize roo
28	108	33.4	192	4	AAB82615	Aab82615 Maize roo
29	108	33.4	192	4	AAB82616	Aab82616 Maize roo
30	108	33.4	192	4	AAG66525	Aag66525 Maize roo
31	108	33.4	192	4	AAG66526	Aag66526 Maize roo
32	106	32.8	168	5	AAU93013	Aau93013 Arabidops
33	106	32.8	168	7	ADD30174	Add30174 Plant yie
34	106	32.8	168	8	ADI43893	Adi43893 Plant tra
35	106	32.8	211	3	AAG08861	Aag08861 Arabidops
36	103	31.9	170	8	ADM48147	Adm48147 Polypepti
37	101	31.3	672	8	ADX95805	Adx95805 Plant ful
38	100.5	31.1	185	9	ADW17162	Adw17162 Eucalyptu
39	99	30.7	143	3	AAB33151	Aab33151 Pinus rad
40	99	30.7	163	9	ADW17580	Adw17580 Pinus rad
41	94	29.1	646	7	ABM86095	Abm86095 Rice abio
42	93	28.8	120	3	AAG27808	Aag27808 Arabidops
43	93	28.8	135	3	AAG07181	Aag07181 Arabidops
44	93	28.8	149	3	AAG07180	Aag07180 Arabidops
45	93	28.8	149	3	AAG27807	Aag27807 Arabidops

ALIGNMENTS

RESULT 1

AAE15373

ID AAE15373 standard; protein; 64 AA.

XX

AC AAE15373;

XX

DT 29-AUG-2003 (revised)

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:19 ; Search time 169.56 Seconds
(without alignments)
392.788 Million cell updates/sec

Title: US-10-663-450-19_COPY_45_116
Perfect score: 365
Sequence: 1 EEKKPVKKRKSQELPVPK.....SRERKRLEMEKLENEKIQME 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	365	100.0	342	2	Q6W8X2_ASPNG	Q6w8x2 aspergillus
2	361	98.9	348	2	Q2U743_ASPOR	Q2u743 aspergillus
3	358	98.1	433	2	Q4WEY8_ASPFU	Q4wey8 aspergillus
4	351	96.2	347	2	Q5AQN3_EMENI	Q5aqn3 aspergillus

5	351	96.2	350	2	Q8TFU8_EMENI	Q8tfu8 emericella
6	298	81.6	451	2	Q8TFF3_TRIRE	Q8tff3 trichoderma
7	297	81.4	430	2	Q7SHF0_NEUCR	Q7shf0 neurospora
8	270	74.0	556	2	Q2KH12_MAGGR	Q2kh12 magnaporthe
9	261	71.5	429	2	Q4HTT5_GIBZE	Q4htt5 gibberella
10	179.5	49.2	299	2	Q6CEV1_YARLI	Q6cev1 yarrowia li
11	177	48.5	357	2	Q5AA52_CANAL	Q5aa52 candida alb
12	175.5	48.1	273	2	Q6CKQ1_KLULA	Q6ckq1 kluyveromyc
13	174	47.7	260	2	Q6BQC2_DEBHA	Q6bqc2 debaryomyce
14	172.5	47.3	230	1	HAC1_YEAST	P41546 saccharomyc
15	168	46.0	228	2	Q75BQ5_ASHGO	Q75bq5 ashbya goss
16	145	39.7	329	2	Q6FLY3_CANGA	Q6fly3 candida gla
17	123	33.7	168	1	HY5_ARATH	O24646 arabidopsis
18	118	32.3	336	2	Q5VR11_ORYSA	Q5vr11 oryza sativ
19	116	31.8	69	2	Q58L60_BRACM	Q58l60 brassica ca
20	116	31.8	109	2	Q84XX8_BRARP	Q84xx8 brassica ra
21	114.5	31.4	252	2	Q6NX18_XENTR	Q6nx18 xenopus tro
22	113.5	31.1	254	2	Q2TAU5_XENLA	Q2tau5 xenopus lae
23	113.5	31.1	350	2	Q90ZR7_XENLA	Q90zr7 xenopus lae
24	113.5	31.1	396	2	Q7ZYC2_XENLA	Q7zyc2 xenopus lae
25	107	29.3	176	2	Q69XK6_ORYSA	Q69xk6 oryza sativ
26	106	29.0	261	2	Q3SZZ2_BOVIN	Q3szz2 bos taurus
27	105	28.8	158	1	HY5_LYCES	Q9sm50 lycopersico
28	105	28.8	703	2	Q4WC74_ASPFU	Q4wc74 aspergillus
29	104	28.5	627	2	Q5BD44_EMENI	Q5bd44 aspergillus
30	103.5	28.4	208	2	Q5DFK2_SCHJA	Q5dfk2 schistosoma
31	103	28.2	263	2	Q8UVQ5_BRARE	Q8uvq5 brachydanio
32	103	28.2	263	2	Q90X27_BRARE	Q90x27 brachydanio
33	103	28.2	383	2	Q8QHJ5_BRARE	Q8qhj5 brachydanio
34	103	28.2	383	2	Q90XD3_BRARE	Q90xd3 brachydanio
35	102.5	28.1	141	2	Q677A7_HYAOR	Q677a7 hyacinthus
36	102.5	28.1	260	2	Q6EZA7_OREMO	Q6eza7 oreochromis
37	102.5	28.1	260	2	Q6EZA8_OREMO	Q6eza8 oreochromis
38	102.5	28.1	261	2	Q3LFR3_FUGRU	Q3lfr3 fugu rubrip
39	102	27.9	321	2	Q8GRY7_LOTJA	Q8gry7 lotus japon
40	101.5	27.8	309	2	Q4H2M2_CIOIN	Q4h2m2 ciona intes
41	101.5	27.8	385	2	Q4RTW2_TETNG	Q4rtw2 tetraodon n
42	101	27.7	261	1	XBP1_HUMAN	P17861 homo sapien
43	100	27.4	267	1	XBP1_RAT	Q9rls4 rattus norv
44	99	27.1	188	2	Q6ZHT8_ORYSA	Q6zht8 oryza sativ
45	98	26.8	267	1	XBP1_MOUSE	O35426 mus musculu

ALIGNMENTS

RESULT 1

Q6W8X2_ASPNG

ID Q6W8X2_ASPNG PRELIMINARY; PRT; 342 AA.

AC Q6W8X2;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 9.

DE Transcription factor HACA.

GN Name=hacA;

OS Aspergillus niger.

OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

OX NCBI_TaxID=5061;

RN [1]

RP NUCLEOTIDE SEQUENCE.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:33:51 ; Search time 20.88 Seconds
(without alignments)
331.782 Million cell updates/sec

Title: US-10-663-450-19_COPY_45_116
Perfect score: 365
Sequence: 1 EEKKPVKKRKSQELPVPK.....SRERKRLEMEKLENEKIOME 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	172.5	47.3	238	2	S78571	transcription fact
2	123	33.7	168	2	T50922	bZIP protein HY5 [
3	100	27.4	267	2	JC4857	hepatocarcinogenes
4	98	26.8	266	2	JC7300	tax-responsive ele
5	98	26.8	322	2	T08592	TGACG-motif-bindin
6	98	26.8	326	2	T08591	TGACG-motif bindin
7	97.5	26.7	260	1	A36299	transcription fact
8	95	26.0	322	2	T12093	TGACG-motif bindin

9	94.5	25.9	506	2	D84609	hypothetical prote
10	89.5	24.5	600	2	T00759	hypothetical prote
11	88.5	24.2	452	2	H96710	hypothetical prote
12	88	24.1	338	1	TVMSFB	transforming prote
13	88	24.1	338	2	I53043	transforming prote
14	87.5	24.0	176	2	B90087	hypothetical prote
15	87.5	24.0	737	2	T15597	hypothetical prote
16	87.5	24.0	849	1	S64732	scaffold attachmen
17	87.5	24.0	1017	2	T15598	hypothetical prote
18	87	23.8	1549	1	A40691	trichohyalin - she
19	85.5	23.4	688	2	T32750	hypothetical prote
20	85	23.3	468	2	S33222	transcription fact
21	85	23.3	1240	2	S52734	hypothetical prote
22	84.5	23.2	246	2	T12585	Dc3 promoter-bindi
23	83.5	22.9	486	2	JC4028	activating transcr
24	82.5	22.6	332	2	S15347	transcription fact
25	82.5	22.6	351	2	A45377	transcription fact
26	82.5	22.6	360	2	T03373	probable G-box bin
27	82.5	22.6	515	2	A42140	box B-binding fact
28	82.5	22.6	516	2	A44494	cAMP-responsive el
29	82	22.5	381	2	S26812	transcription fact
30	81.5	22.3	774	2	S25284	protein kinase nek
31	81	22.2	349	2	A41349	histone-specific t
32	81	22.2	349	2	S77570	transcription fact
33	81	22.2	433	2	JC1230	DNA-binding protei
34	80.5	22.1	839	2	I50590	class I INCENP pro
35	80.5	22.1	877	2	I50591	class II INCENP pr
36	80	21.9	313	2	A34785	DNA-binding protei
37	80	21.9	331	2	S33223	transcription fact
38	80	21.9	358	2	C42026	cyclic AMP respons
39	80	21.9	389	1	A39429	cAMP response elem
40	80	21.9	448	2	A42026	cAMP response elem
41	80	21.9	456	2	B42026	cyclic AMP respons
42	80	21.9	505	1	S05380	transcription fact
43	80	21.9	771	1	A33430	h-caldesmon - chic
44	79.5	21.8	372	2	S17715	transcription acti
45	79.5	21.8	483	2	S12741	transcription fact

ALIGNMENTS

RESULT 1

S78571

transcription factor HAC1 - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein YFL031w

C;Species: *Saccharomyces cerevisiae*

C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004

C;Accession: S78571; S56223; S53578

R;Murakami, Y.

submitted to the Protein Sequence Database, January 1998

A;Reference number: S78570

A;Accession: S78571

A;Molecule type: DNA

A;Residues: 1-238

A;Cross-references: UNIPROT:P41546; UNIPARC:UPI0000157F61; EMBL:D50617; MIPS:YFL031w

A;Note: this is a revision to the sequence from reference S56186

R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasa submitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from *Saccaromyces*

A;Reference number: S56186

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450-19_copy_45_116.rapbn.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:44:20 ; Search time 9.72 Seconds
(without alignments)
169.226 Million cell updates/sec

Title: US-10-663-450-19_COPY_45_116
Perfect score: 365
Sequence: 1 EEKKPVKKRKSWGQELPVPK.....SRERKRLEMEKLENEKIQME 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 99297 seqs, 22845552 residues

Total number of hits satisfying chosen parameters: 99297

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
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4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query
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No.	Score	Match Length	DB	ID	Description	
1	275	75.3	425	6	US-10-449-902-40262	Sequence 40262, A
2	108	29.6	134	6	US-10-953-349-13422	Sequence 13422, A
3	108	29.6	134	6	US-10-953-349-22329	Sequence 22329, A
4	108	29.6	191	6	US-10-953-349-13421	Sequence 13421, A
5	108	29.6	191	6	US-10-953-349-22328	Sequence 22328, A
6	98	26.8	199	6	US-10-953-349-12209	Sequence 12209, A
7	98	26.8	201	6	US-10-953-349-20562	Sequence 20562, A
8	98	26.8	318	6	US-10-953-349-12208	Sequence 12208, A
9	98	26.8	320	6	US-10-953-349-20561	Sequence 20561, A
10	98	26.8	324	6	US-10-953-349-12207	Sequence 12207, A
11	98	26.8	326	6	US-10-953-349-20560	Sequence 20560, A
12	95.5	26.2	646	6	US-10-449-902-51369	Sequence 51369, A
13	90.5	24.8	293	6	US-10-953-349-23767	Sequence 23767, A
14	90.5	24.8	318	6	US-10-953-349-23766	Sequence 23766, A
15	90.5	24.8	323	6	US-10-953-349-23765	Sequence 23765, A
16	89.5	24.5	335	6	US-10-449-902-34705	Sequence 34705, A
17	88	24.1	467	7	US-11-293-697-3606	Sequence 3606, Ap
18	88	24.1	611	7	US-11-321-421-81	Sequence 81, Appl
19	87.5	24.0	675	7	US-11-293-697-3326	Sequence 3326, Ap
20	81.5	22.3	296	6	US-10-953-349-24027	Sequence 24027, A
21	81.5	22.3	362	6	US-10-953-349-24026	Sequence 24026, A
22	81.5	22.3	382	6	US-10-953-349-24025	Sequence 24025, A
23	81.5	22.3	467	6	US-10-449-902-38097	Sequence 38097, A
24	81	22.2	332	6	US-10-953-349-23520	Sequence 23520, A
25	81	22.2	457	6	US-10-449-902-53115	Sequence 53115, A
26	81	22.2	523	6	US-10-449-902-56056	Sequence 56056, A
27	81	22.2	650	6	US-10-449-902-44708	Sequence 44708, A
28	80	21.9	142	6	US-10-449-902-31867	Sequence 31867, A
29	79.5	21.8	675	6	US-10-449-902-42244	Sequence 42244, A
30	78.5	21.5	539	6	US-10-449-902-54234	Sequence 54234, A
31	78	21.4	147	6	US-10-953-349-36806	Sequence 36806, A
32	78	21.4	165	6	US-10-953-349-36805	Sequence 36805, A
33	78	21.4	186	6	US-10-953-349-36804	Sequence 36804, A
34	77.5	21.2	437	6	US-10-449-902-40619	Sequence 40619, A
35	77	21.1	484	6	US-10-449-902-47431	Sequence 47431, A
36	77	21.1	484	6	US-10-449-902-55580	Sequence 55580, A
37	76	20.8	215	6	US-10-449-902-45271	Sequence 45271, A
38	76	20.8	301	6	US-10-449-902-43842	Sequence 43842, A
39	75.5	20.7	281	6	US-10-971-483-2	Sequence 2, Appli
40	75.5	20.7	357	6	US-10-449-902-44625	Sequence 44625, A
41	75.5	20.7	380	6	US-10-449-902-43338	Sequence 43338, A
42	75.5	20.7	577	7	US-11-289-102-220	Sequence 220, App
43	75	20.5	167	6	US-10-449-902-40094	Sequence 40094, A
44	75	20.5	253	6	US-10-953-349-11914	Sequence 11914, A
45	75	20.5	334	6	US-10-449-902-53341	Sequence 53341, A

ALIGNMENTS

RESULT 1

US-10-449-902-40262

; Sequence 40262, Application US/10449902

; Publication No. US20060123505A1

; GENERAL INFORMATION:

; APPLICANT: National Institute of Agrobiological Sciences.

; APPLICANT: Bio-oriented Technology Research Advancement Institution.

; APPLICANT: The Institute of Physical and Chemical Research.

; APPLICANT: Foundation for Advancement of International Science.

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450- 19_copy_45_116.rapbm.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:42:39 ; Search time 113.4 Seconds
(without alignments)
294.105 Million cell updates/sec

Title: US-10-663-450-19_COPY_45_116
Perfect score: 365
Sequence: 1 EEKKPVKKRKSWSQELPVPK.....SRERKRLEMEKLENEKIOME 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	365	100.0	386	3	US-09-816-277-16	Sequence 16, Appl
4	365	100.0	386	4	US-10-663-450-16	Sequence 16, Appl
5	351	96.2	349	3	US-09-816-277-4	Sequence 4, Appli
6	351	96.2	349	3	US-09-816-277-6	Sequence 6, Appli
7	351	96.2	349	4	US-10-663-450-4	Sequence 4, Appli
8	351	96.2	349	4	US-10-663-450-6	Sequence 6, Appli
9	298	81.6	451	3	US-09-816-277-2	Sequence 2, Appli
10	298	81.6	451	3	US-09-816-277-5	Sequence 5, Appli
11	298	81.6	451	4	US-10-663-450-2	Sequence 2, Appli
12	298	81.6	451	4	US-10-663-450-5	Sequence 5, Appli
13	295	80.8	409	3	US-09-533-029-104	Sequence 104, App
14	295	80.8	409	4	US-10-295-403-158	Sequence 158, App
15	295	80.8	409	4	US-10-412-699B-684	Sequence 684, App
16	271	74.2	174	4	US-10-767-701-61238	Sequence 61238, A
17	172.5	47.3	200	4	US-10-369-493-21867	Sequence 21867, A
18	171	46.8	68	3	US-09-816-277-60	Sequence 60, Appl
19	171	46.8	68	4	US-10-663-450-60	Sequence 60, Appl
20	123	33.7	168	3	US-09-934-455-102	Sequence 102, App
21	123	33.7	168	4	US-10-225-066A-206	Sequence 206, App
22	123	33.7	168	4	US-10-374-780A-2356	Sequence 2356, Ap
23	123	33.7	168	5	US-10-732-923-13692	Sequence 13692, A
24	123	33.7	168	5	US-10-225-066A-206	Sequence 206, App
25	118	32.3	203	4	US-10-437-963-151695	Sequence 151695,
26	118	32.3	203	5	US-10-732-923-13694	Sequence 13694, A
27	118	32.3	203	5	US-10-732-923-13695	Sequence 13695, A
28	116	31.8	109	5	US-10-732-923-13697	Sequence 13697, A
29	113	31.0	147	4	US-10-425-115-187302	Sequence 187302,
30	110.5	30.3	192	3	US-09-772-656-2	Sequence 2, Appli
31	110.5	30.3	192	3	US-09-772-656-6	Sequence 6, Appli
32	110.5	30.3	192	3	US-09-772-656-10	Sequence 10, Appl
33	110.5	30.3	192	4	US-10-396-199A-2	Sequence 2, Appli
34	110.5	30.3	192	4	US-10-396-199A-6	Sequence 6, Appli
35	110.5	30.3	192	4	US-10-396-199A-10	Sequence 10, Appl
36	109	29.9	143	5	US-10-856-499-1930	Sequence 1930, Ap
37	108	29.6	196	4	US-10-425-115-197786	Sequence 197786,
38	107	29.3	176	4	US-10-437-963-164243	Sequence 164243,
39	105.5	28.9	170	4	US-10-310-154-565	Sequence 565, App
40	104.5	28.6	168	4	US-10-425-115-246428	Sequence 246428,
41	103.5	28.4	191	4	US-10-424-599-177263	Sequence 177263,
42	103	28.2	181	5	US-10-732-923-450	Sequence 450, App
43	101.5	27.8	114	4	US-10-425-115-246430	Sequence 246430,
44	101	27.7	217	4	US-10-425-115-197783	Sequence 197783,
45	101	27.7	261	4	US-10-205-823-453	Sequence 453, App

ALIGNMENTS

RESULT 1

US-09-816-277-19

; Sequence 19, Application US/09816277

; Publication No. US20010034045A1

; GENERAL INFORMATION:

; APPLICANT: Penttila, Merja E.

; APPLICANT: Ward, Michael

; APPLICANT: Wang, Huaming

; APPLICANT: Valkonen, Mari J.

; APPLICANT: Saloheimo, Markku

; TITLE OF INVENTION: Increased Production of Secreted

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-450- 19_copy_45_116.rai.

Score Home Page	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:41:45 ; Search time 33.12 Seconds
(without alignments)
190.284 Million cell updates/sec

Title: US-10-663-450-19_COPY_45_116
Perfect score: 365
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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2	177	48.5	248	2	US-09-248-796A-18840	Sequence 18840, A
3	109	29.9	143	2	US-09-640-211A-1930	Sequence 1930, Ap
4	101	27.7	264	2	US-09-949-016-10789	Sequence 10789, A
5	100.5	27.5	102	2	US-09-640-211A-1046	Sequence 1046, Ap
6	97.5	26.7	260	2	US-09-538-092-950	Sequence 950, App
7	88	24.1	338	1	US-08-218-686-2	Sequence 2, Appli
8	88	24.1	338	2	US-08-460-242-2	Sequence 2, Appli
9	88	24.1	452	2	US-09-949-016-7289	Sequence 7289, Ap
10	88	24.1	611	2	US-09-216-393B-81	Sequence 81, Appl
11	88	24.1	1637	2	US-09-718-692-2	Sequence 2, Appli
12	88	24.1	1637	2	US-09-718-852-2	Sequence 2, Appli
13	88	24.1	1637	2	US-09-718-815-2	Sequence 2, Appli
14	87.5	24.0	931	2	US-09-949-016-9850	Sequence 9850, Ap
15	85.5	23.4	472	2	US-09-520-781-22	Sequence 22, Appl
16	85.5	23.4	472	2	US-09-957-187-22	Sequence 22, Appl
17	85.5	23.4	472	2	US-09-991-053-22	Sequence 22, Appl
18	85.5	23.4	491	2	US-09-520-781-24	Sequence 24, Appl
19	85.5	23.4	491	2	US-09-957-187-24	Sequence 24, Appl
20	85.5	23.4	491	2	US-09-991-053-24	Sequence 24, Appl
21	85.5	23.4	521	1	US-08-721-684C-2	Sequence 2, Appli
22	85.5	23.4	521	1	US-09-005-970-2	Sequence 2, Appli
23	85.5	23.4	521	2	US-09-407-715-2	Sequence 2, Appli
24	85	23.3	1240	2	US-09-538-092-658	Sequence 658, App
25	84	23.0	667	2	US-09-248-796A-14492	Sequence 14492, A
26	83	22.7	23	2	US-09-831-642-72	Sequence 72, Appl
27	82.5	22.6	307	2	US-09-267-031-6	Sequence 6, Appli
28	82.5	22.6	351	2	US-09-870-089B-2	Sequence 2, Appli
29	82.5	22.6	362	2	US-09-949-016-10923	Sequence 10923, A
30	81.5	22.3	118	2	US-09-134-001C-2856	Sequence 2856, Ap
31	81.5	22.3	616	2	US-09-873-404-4	Sequence 4, Appli
32	81.5	22.3	616	2	US-10-243-735-4	Sequence 4, Appli
33	81.5	22.3	616	2	US-10-730-010-4	Sequence 4, Appli
34	81.5	22.3	802	2	US-09-823-240A-2	Sequence 2, Appli
35	81	22.2	422	2	US-09-248-796A-19321	Sequence 19321, A
36	80.5	22.1	470	2	US-10-104-047-3775	Sequence 3775, Ap
37	80.5	22.1	483	2	US-09-949-016-7773	Sequence 7773, Ap
38	80.5	22.1	603	2	US-10-094-749-1914	Sequence 1914, Ap
39	80.5	22.1	1034	2	US-09-976-594-590	Sequence 590, App
40	80	21.9	63	2	US-09-107-433-3674	Sequence 3674, Ap
41	80	21.9	501	2	US-09-949-016-11281	Sequence 11281, A
42	79.5	21.8	235	2	US-09-270-767-36681	Sequence 36681, A
43	79.5	21.8	235	2	US-09-270-767-51898	Sequence 51898, A
44	79	21.6	170	2	US-09-248-796A-27838	Sequence 27838, A
45	79	21.6	325	2	US-09-267-031-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1

US-09-533-029-104

; Sequence 104, Application US/09533029

; Patent No. 6664446

; GENERAL INFORMATION:

; APPLICANT: Heard, Jacqueline

; APPLICANT: Broun, Pierre

; APPLICANT: Riechmann, Jose-Luis

; APPLICANT: Keddie, James

; APPLICANT: Pineda, Omaira

SCORE Search Results Details for Application 10663450 and Search Result us-10-663-45- 19_copy_45_116.rag.

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OM protein - protein search, using sw model

Run on: June 28, 2006, 01:26:15 ; Search time 149.76 Seconds
(without alignments)
219.816 Million cell updates/sec

Title: US-10-663-450-19_COPY_45_116
Perfect score: 365
Sequence: 1 EEKKPVKKRKSQGLPVPK.....SRERKRLEMEKLENEKIQME 72

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	365	100.0	342	4	AAB82977	Aab82977 Aspergill
2	365	100.0	342	5	AAE15381	Aae15381 Aspergill
3	365	100.0	342	8	ADS12818	Ads12818 Aspergill
4	365	100.0	386	5	AAE15379	Aae15379 Aspergill
5	365	100.0	386	8	ADS12815	Ads12815 Aspergill
6	351	96.2	349	8	ADS12805	Ads12805 Aspergill
7	351	96.2	349	8	ADS12803	Ads12803 Aspergill
8	351	96.2	349	8	ADS12863	Ads12863 Aspergill
9	351	96.2	350	4	AAB82976	Aab82976 Aspergill
10	351	96.2	350	5	AAE15372	Aae15372 Aspergill
11	321	87.9	64	5	AAE15374	Aae15374 Aspergill
12	298	81.6	450	4	AAB82975	Aab82975 Trichoder
13	298	81.6	451	5	AAE15371	Aae15371 Trichoder
14	298	81.6	451	8	ADS12801	Ads12801 Trichoder
15	298	81.6	451	8	ADS12804	Ads12804 Trichoder
16	295	80.8	409	7	ABO43144	Abo43144 A. thalia
17	295	80.8	409	7	ADB31925	Adb31925 Plant (A.
18	295	80.8	409	8	ADO02271	Ado02271 Thalecres
19	292	80.0	64	5	AAE15373	Aae15373 Trichoder
20	172.5	47.3	84	5	ABP02534	Abp02534 Human ORF
21	172.5	47.3	200	8	ADS43437	Ads43437 Bacterial
22	172.5	47.3	230	2	AAW53806	Aaw53806 Transcrip
23	172.5	47.3	230	8	ADT87049	Adt87049 Yeast Str
24	172.5	47.3	238	2	AAW53807	Aaw53807 Transcrip
25	171	46.8	68	5	AAE15382	Aae15382 Yeast HAC
26	171	46.8	68	8	ADS12859	Ads12859 Saccharom
27	123	33.7	168	5	AAU93013	Aau93013 Arabidops
28	123	33.7	168	7	ADD30174	Add30174 Plant yie
29	123	33.7	168	8	ADI43893	Adi43893 Plant tra
30	123	33.7	211	3	AAG08861	Aag08861 Arabidops
31	110.5	30.3	192	4	AAB82614	Aab82614 Maize roo
32	110.5	30.3	192	4	AAB82615	Aab82615 Maize roo
33	110.5	30.3	192	4	AAB82616	Aab82616 Maize roo
34	110.5	30.3	192	4	AAG66525	Aag66525 Maize roo
35	110.5	30.3	192	4	AAG66526	Aag66526 Maize roo
36	109.5	30.0	185	9	ADW17162	Adw17162 Eucalyptu
37	109	29.9	143	3	AAB33151	Aab33151 Pinus rad
38	108	29.6	163	9	ADW17580	Adw17580 Pinus rad
39	105.5	28.9	170	8	ADM48147	Adm48147 Polypepti
40	101	27.7	261	6	ABR47631	Abr47631 Breast ca
41	101	27.7	261	7	ADB75629	Adb75629 Prostate
42	101	27.7	261	8	ADL83138	Adl83138 Human PRO
43	101	27.7	261	8	ADN16846	Adn16846 Human XB1
44	101	27.7	261	8	ADR14692	Adr14692 Human NF-
45	101	27.7	261	8	ABM82329	Abm82329 Tumour-as

ALIGNMENTS

RESULT 1

AAB82977

ID AAB82977 standard; protein; 342 AA.

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AC AAB82977;

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DT 11-SEP-2003 (revised)